Measuring Heritability and the Classic Twin Design

Dr Angelica Ronald,

Genes Environment Lifespan laboratory,
Birkbeck, London

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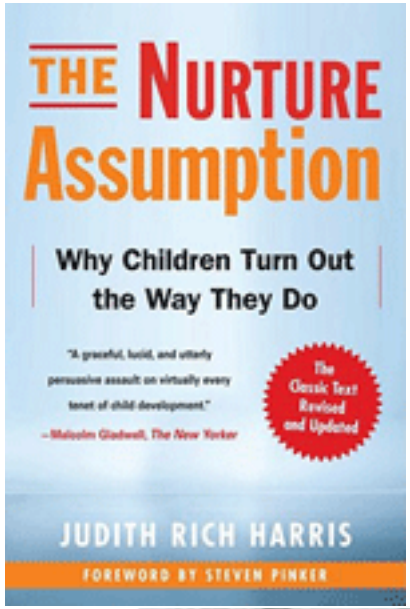
Genetics for Social Scientists, LSHTM

www.gel.bbk.ac.uk

Outline

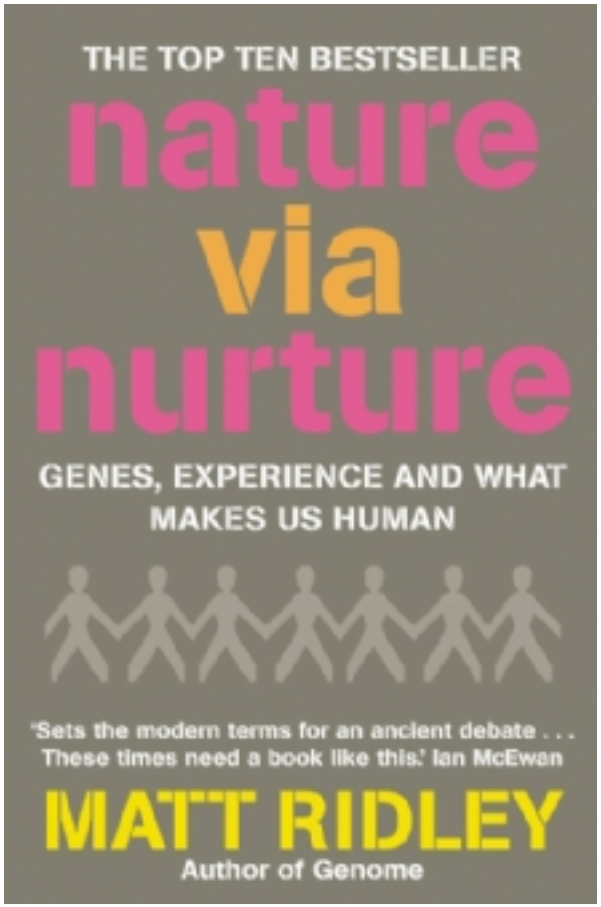
- Background
- Sibling recurrence risk ratio
- The classic twin study design
- Heritability
- Environmental influences
- Multivariate extensions of twin analyses
- Assumptions and Limitations

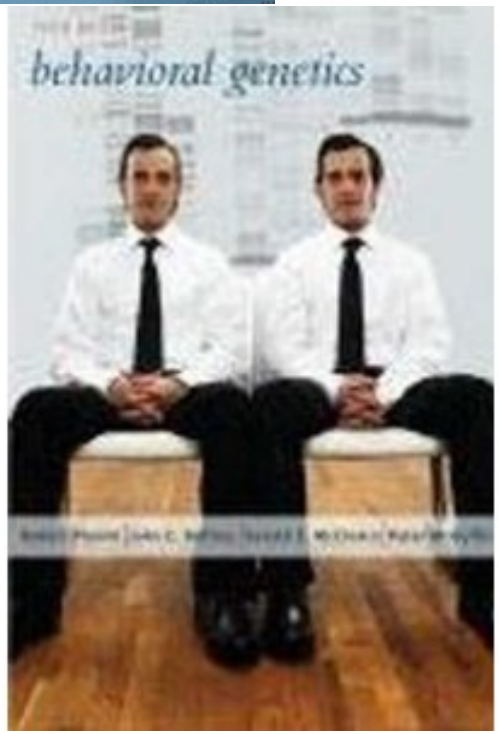
Nature and Nurture

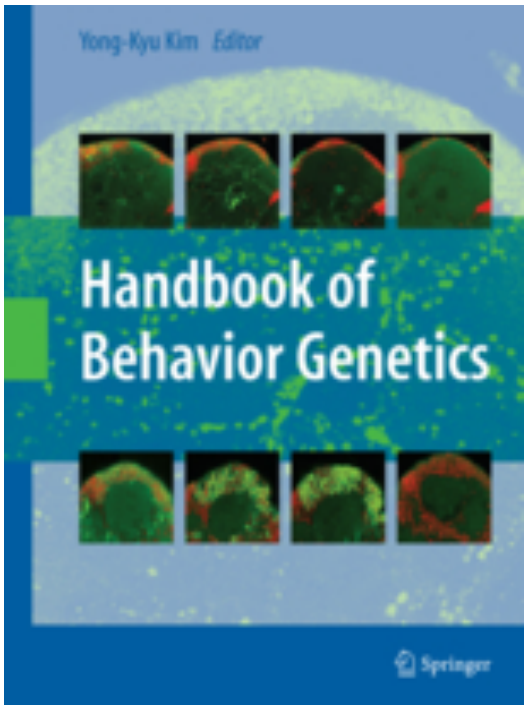


Nature *or* Nurture – WRONG!

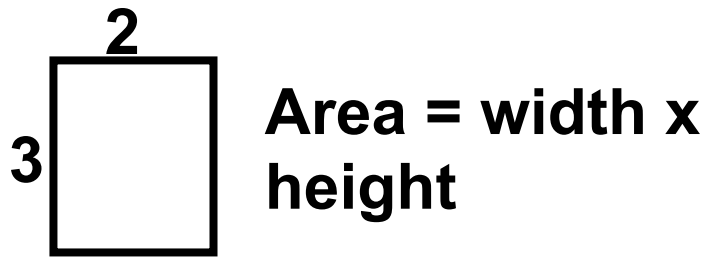
Nature *and* Nurture – neither can exist in isolation!



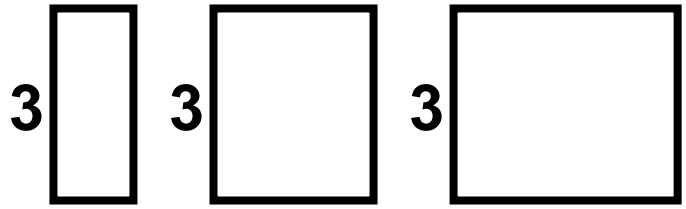




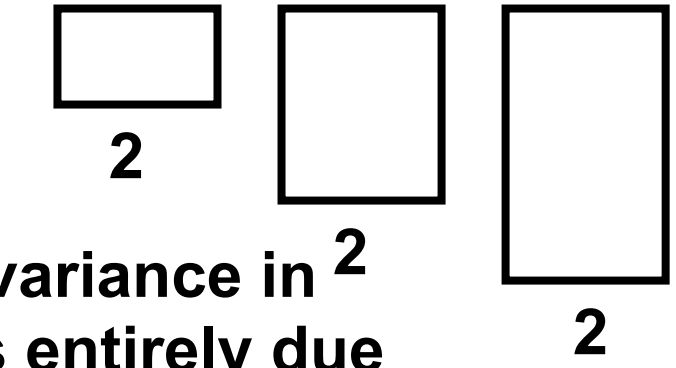
Genes and Environment



Area = width x height



Here, variance in area is entirely due to width



Here, variance in area is entirely due to height

With <u>behaviour</u> there needs to be both an organism (that has genes) and an environment. To what extent do genes and environment influence differences among individuals?

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Sibling recurrence risk ratio, λ_S

- Estimate of familial aggregation of disease
- Definition: Ratio of disease manifestation, given that one's sibling is affected, compared with disease prevalence in the general population
- λ = risk of disease in the relatives of an individual with disease/ population prevalence of disease

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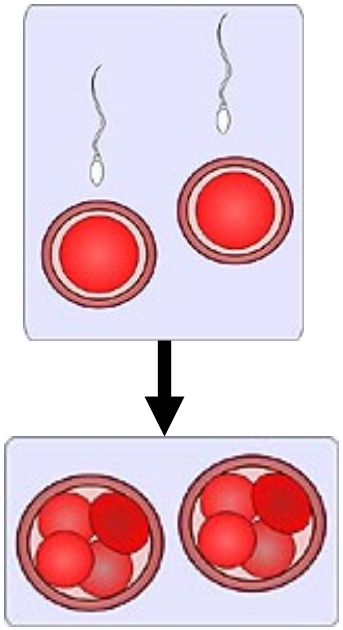
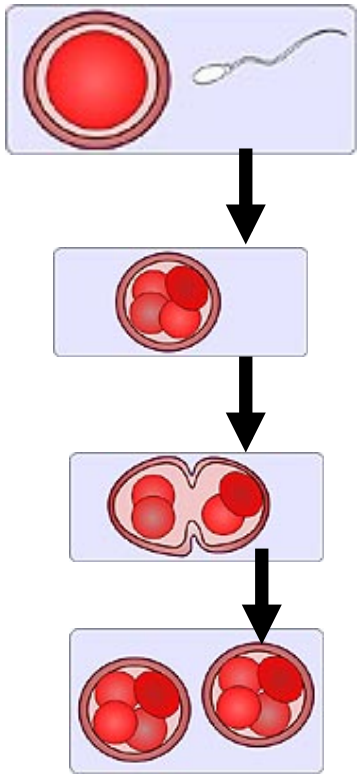
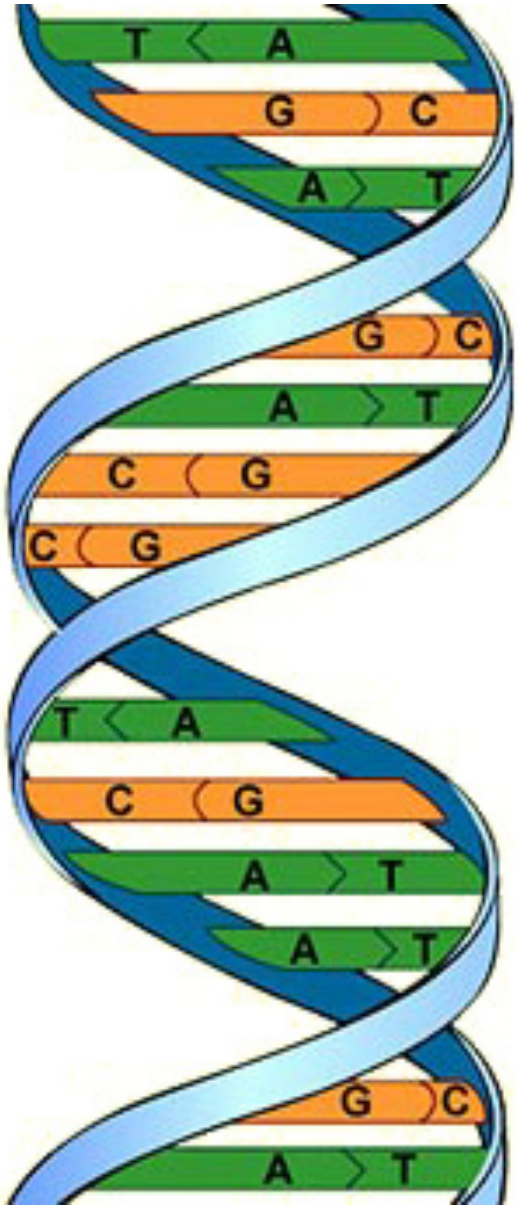
Twin Studies

- Based on the comparison of similarity of identical (monozygotic, MZ) twin pairs and fraternal (dizygotic, DZ) twin pairs







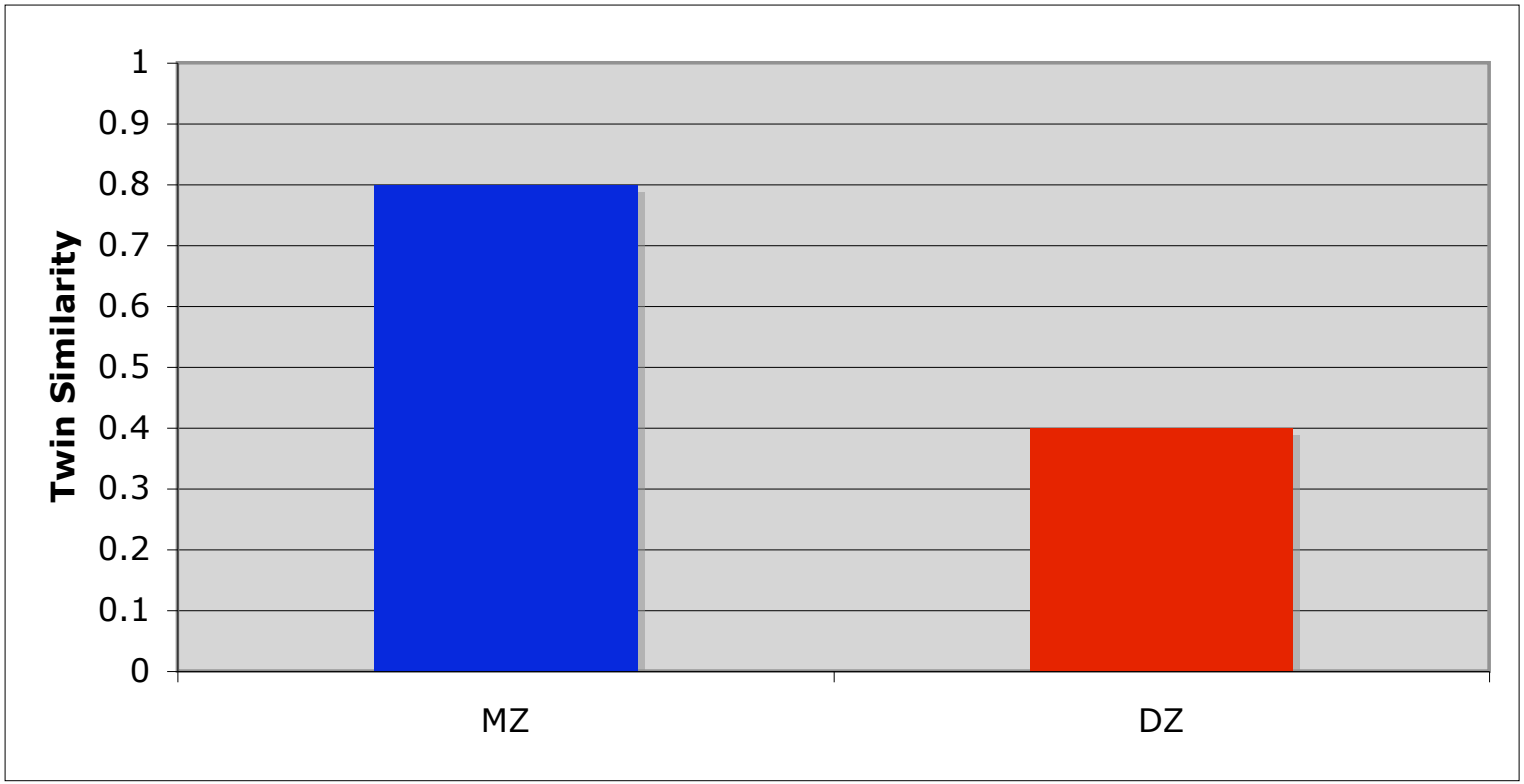
MZ twins share 100% of their DNA code

DZ twins share on average 50% of their DNA code

Twins Early Development Study (TEDS) twins

PI: Professor Robert Plomin

Interpreting Twin Correlations



Interpreting Twin Correlations

$r_{MZ} = h^2$ and c^2

$r_{DZ} = h^2/2$ and c^2

$r_{MZ} - r_{DZ} = h^2 - h^2/2 + c^2 - c^2 = h^2/2$

A or $h^2 = 2(r_{MZ} - r_{DZ})$

C or $c^2 = r_{MZ} - h^2$

E or $e^2 = 1 - r_{MZ}$

r_{MZ} = similarity between monozygotic twins

r_{DZ} = similarity between dizygotic twins

A or h^2 = heritability

C = shared environment estimate

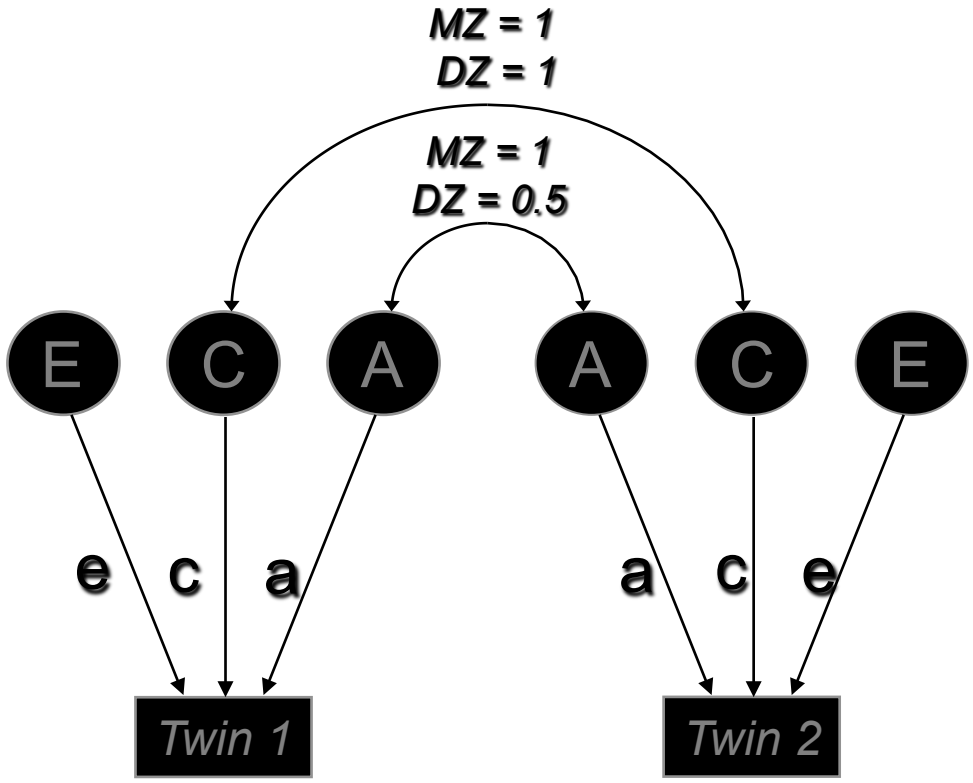
E = nonshared environment estimate

Heritability (h^2) is the proportion of variance of a phenotype explained by genetic influences in a population of individuals

Sources of variance

- **Additive genetic - A**
- **Interaction between alleles at same locus (dominance) or different loci (epistasis) – D**
- **Common environmental influences shared by members of the same family – C**
- **Non-shared environmental influences unique to the individual – E**
- **Measurement error (included in the E term)**

Twin Model-Fitting: Example univariate path diagram



A = additive genetic influences
C = shared environmental influences
E = nonshared environmental influences

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Environmental causes (as defined by behaviour genetics)

- Any influences other than the actual DNA code that contribute to individual differences on a particular phenotype
- i.e. different to the lay meaning of ‘the environment’
- Two types: Shared and Nonshared

Shared Environment

- Influences that make children growing up in the same family similar
- Examples:
  - Socioeconomic status
  - Parenting
  - Characteristics of home (e.g., number of books)

Note distal vs. proximal types

Nonshared Environment

- Influences that make children growing up in the same family different
- Examples:
  - Peers
  - Child-specific illnesses/ events e.g. Bump on the head
  - Events occurring to an individual

Note this term includes variance attributable to measurement error

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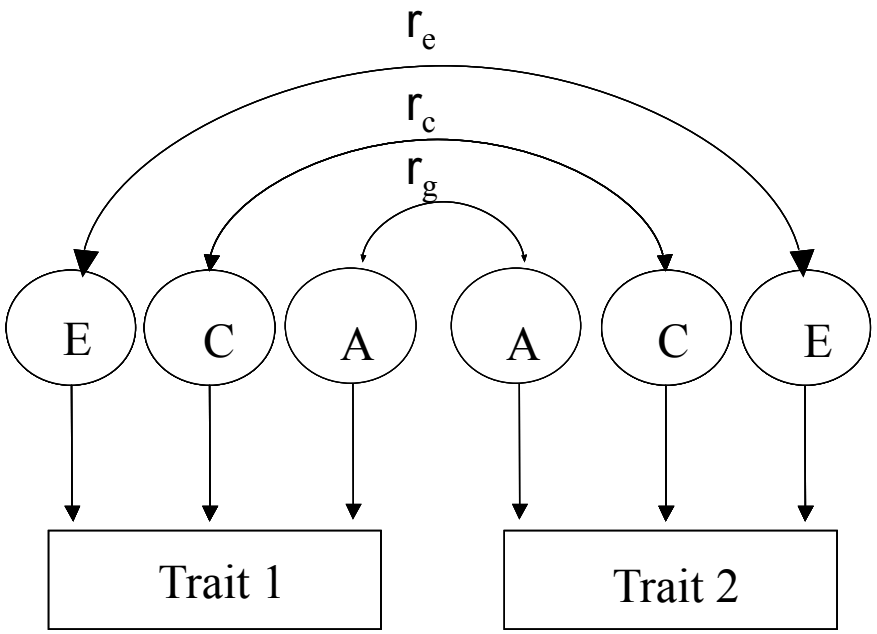
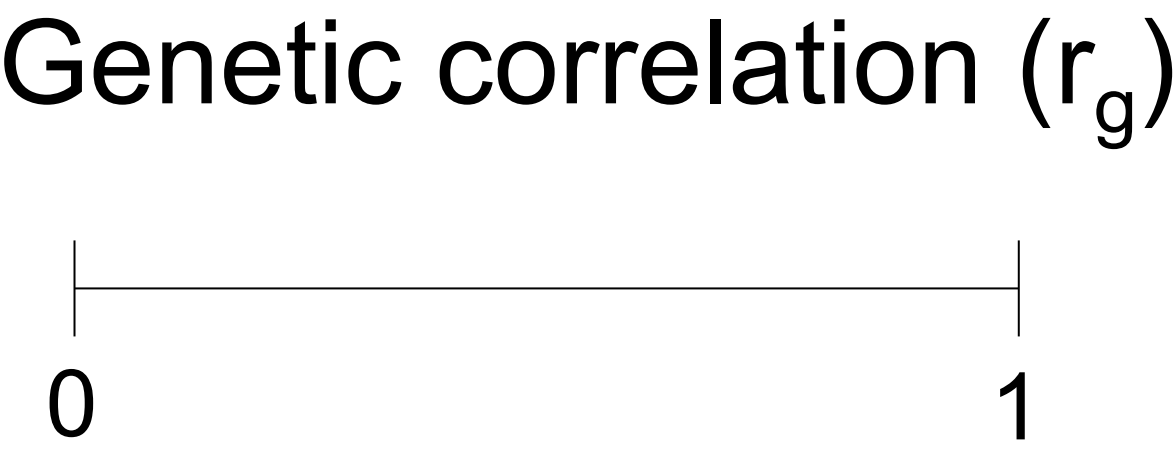
Bivariate twin model



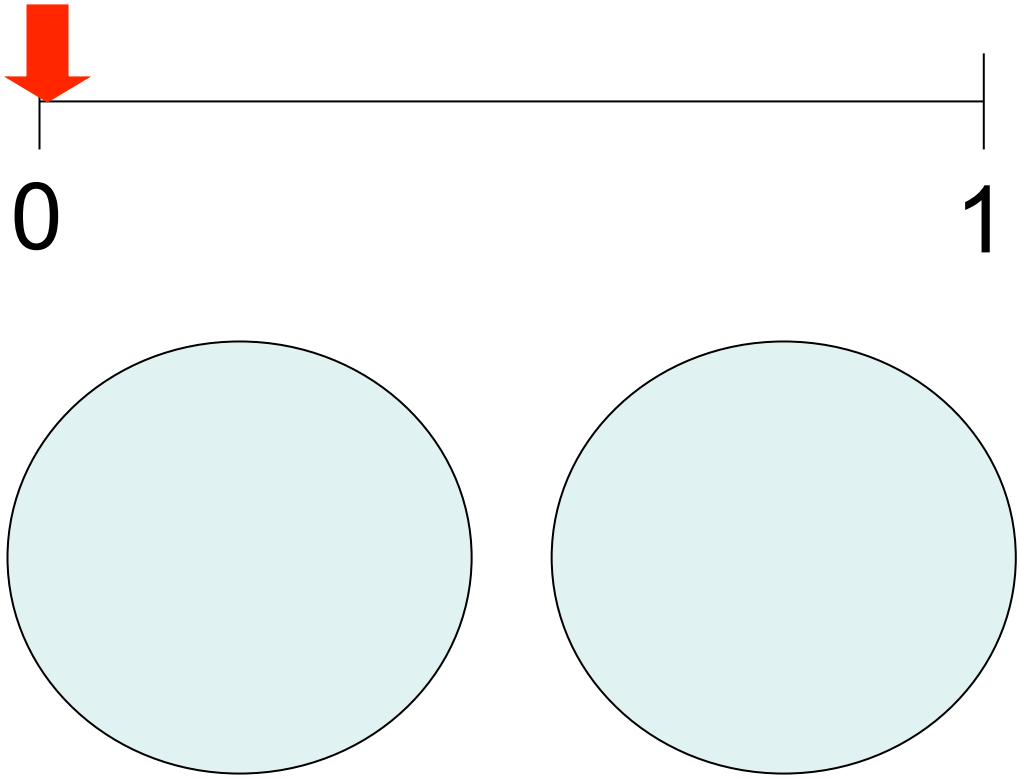
To what extent is trait 1 caused by the same genetic and environmental influences as trait 2?

Genetic correlation (r_g)

- r_g is a statistic derived from bivariate twin models
- r_g is independent of
  - the heritability estimates of either trait
  - the strength of the phenotypic relationship between two traits

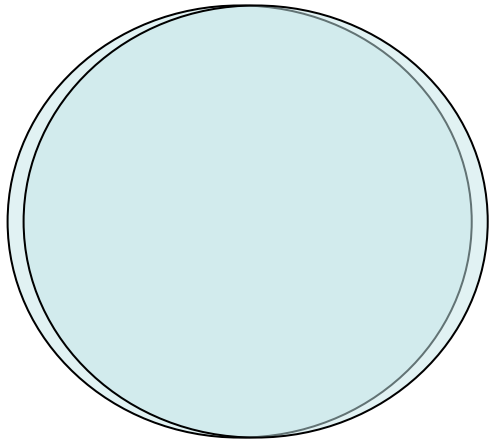

Genetic correlation (r_g)
0
1

Genetic correlation (r_g)



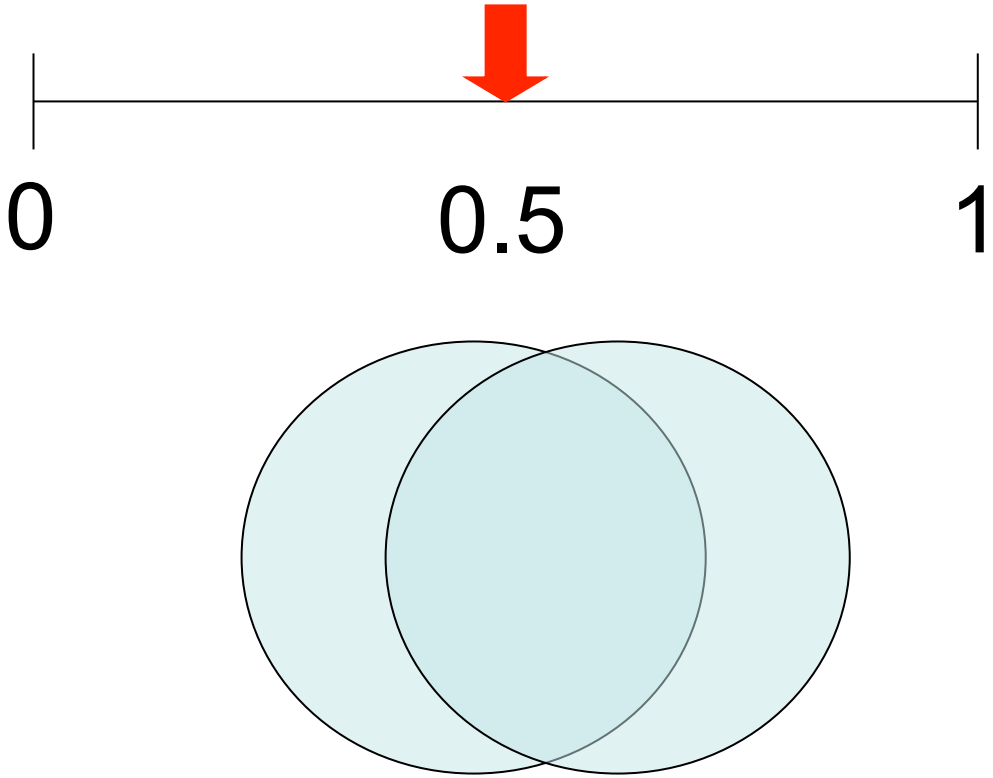
If r_g = 0, there are no common genetic influences across two traits

Genetic correlation (r_g)



If r_g = 1, all the genes influencing the two traits are completely overlapping.
At the genetic level, these two things are the same

Genetic correlation (r_g)



r_g = 0.5, some the genes are overlapping between the two traits, and some are specific to each

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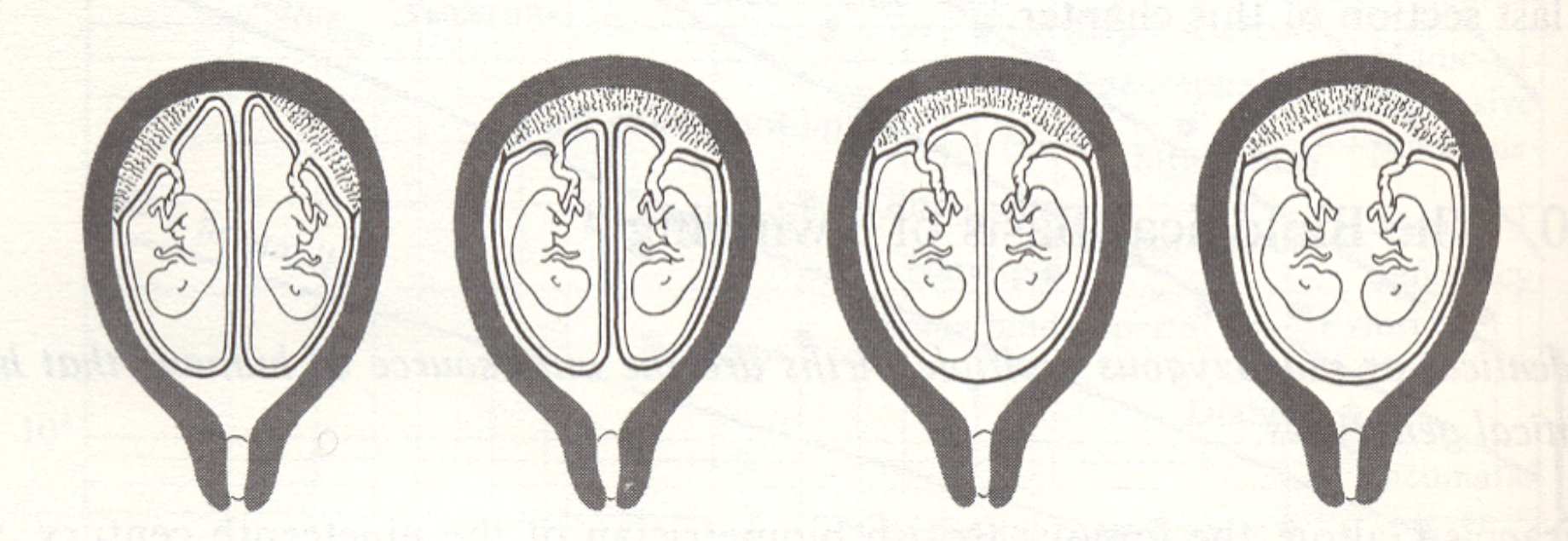
Assumptions of the Twin Design

- Findings from twins are generalisable to singletons
- Assumes no gene-environment correlation or gene-environment interaction
- No effect of chorion or amnion differences
- Equal environments assumption

Chorions and Amions



Equal Environments Assumption

- The EEA posits that environmental influences are equivalent for MZ and DZ twin pairs, that any excess similarity of MZ twins over DZ twins is explained by genetic factors

Evidence:

- Mistaken zygosity
- Effect of physical similarity
- Effect of environment similarity

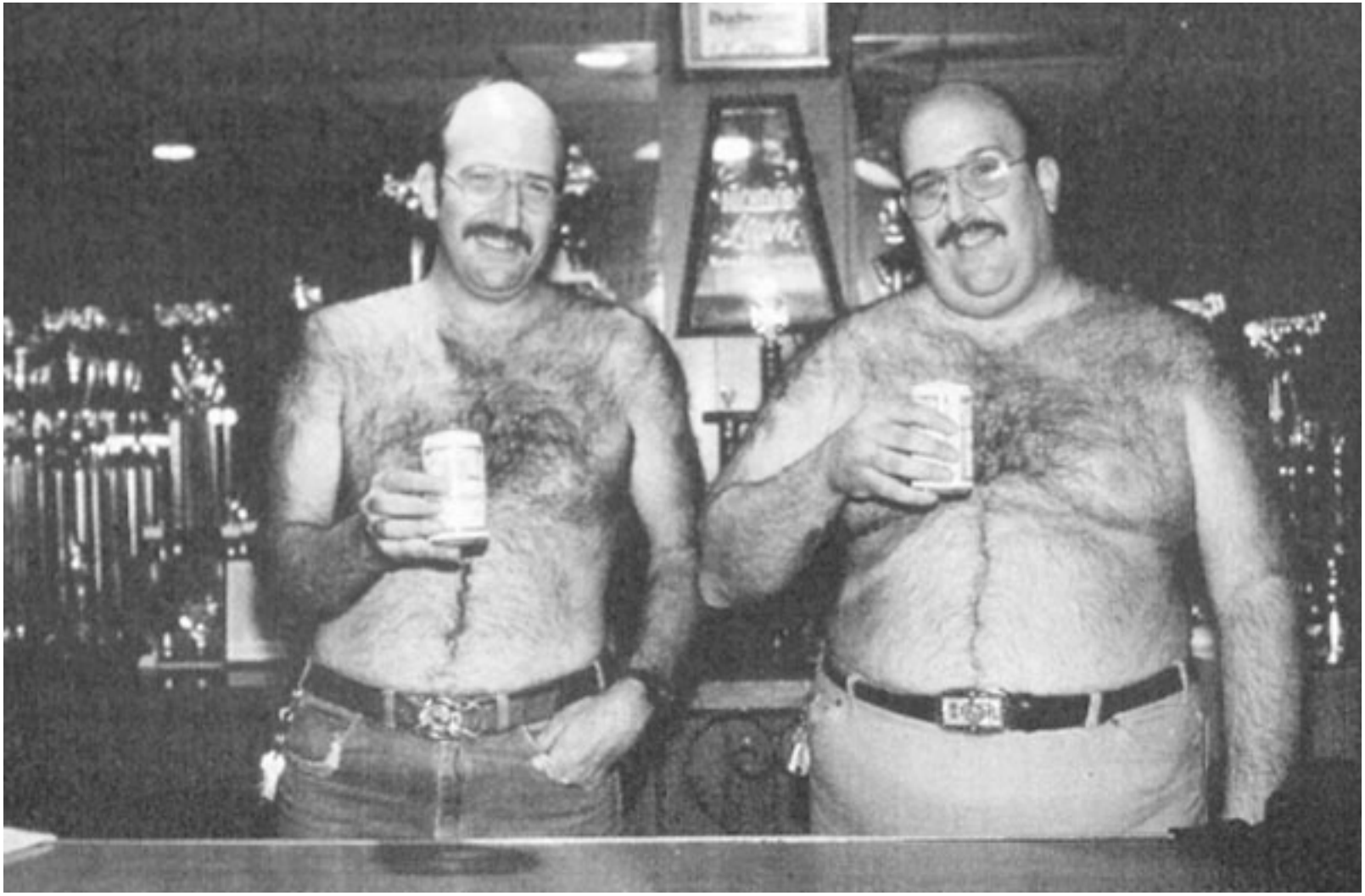
Twin Studies

- Advantages
- Can partition variance into A + C + E
- Reasonably representative of general population
- Willing participants
- Relatively unbiased
- Twin design assumptions mostly supported by data
- Don't need a 'control' group
- All participants are the same age

- Disadvantages
- Require large samples (ideally >1000 pairs) to have power to detect effects
- Design has assumptions (but so do all study designs)
- Some twin-specific characteristics are not generalisable to singletons

Other behaviour genetic research designs

- Family designs
- Adoption designs
- Extended twin designs
- MZ twins reared apart



MZ twins reared apart - note the same way of supporting their cans of beer

Learning Questions

- What are the main differences between monozygotic and dizygotic twins?
- What does heritability mean?
- What are some of the assumptions of the twin design?
- Why would you use multivariate twin analyses?
- In behaviour genetics, what counts as environmental influences?